

SEQUENCE LISTING

<110> MOECKEL, Bettina

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PFEFFERLE, Walter

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<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE

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<150> DE10107229.5

<151> 2001-02-16

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<170> PatentIn version 3.0

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12> PRT

13> Corynebacterium glutamicum

100> 4

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 325 330 335

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 Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
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 Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
 450 455 460
 Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
 465 470 475 480
 Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
 485 490 495
 Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
 500 505 510
 Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
 515 520 525
 Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp
 530 535 540
 Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
 545 550 555 560
 Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
 565 570 575
 Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
 580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr
610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn
625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu
645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr
660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln
675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly
690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu
705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr
725 730 735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu
740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
755 760 765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val
770 775 780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr
785 790 795 800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys
805 810 815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp

835

840

845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys
850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr
1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly
 1085 1090 1095

Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu
 1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser
 1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe
 1130 1135 1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu
 1145 1150 1155

Arg Ser Asp Ala Asp Thr Ala
 1160 1165

210> 5
 211> 5099
 212> DNA
 213> Corynebacterium glutamicum
 220>
 221> CDS
 222> (702)..(4196)

<400> 5
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 aaaatattga tgatttttac ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120
 tcgacgcctc cctcgacgat gcagctgtct ctaagctggg tgcacaggcc gaaagcatcc 180
 ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggg gcggtattgg 240
 ctctcgtggg cctggccggg tgttttgggg cgtttgggaa gaaacgtcga gaagcttaac 300
 ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccggggt tgtttgctag 360
 ggtgcctcgt agaaggggtc aagaagattt ctgggaaacg cgcccgtgcg gttggttgct 420
 aatagcacgc ggagcaccag atgaaaaatc tcccctttac ttctgcgcgc gattggtata 480
 ctctgagtcg ttgcgttgga attcgtgact ctttttcgtt cctgtagcgc caagaccttg 540
 atcaaggtgg tttaaaaaaa ccgatttgac aaggtcattc agtgctatct ggagtcgttc 600

aggggggatcg ggttcctcag cagaccaatt gctcaaaaat accagcgggtg ttgatctgca	660
cttaatggcc ttgaccagcc aggtgcaatt acccgcggtga g gtg ctg gaa gga ccc	716
Val Leu Glu Gly Pro	
1 5	
atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt	764
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly	
10 15 20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg	812
Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val	
25 30 35	
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt	860
Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly	
40 45 50	
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc	908
Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala	
55 60 65	
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc	956
Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile	
70 75 80 85	
gag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc	1004
Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe	
90 95 100	
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac	1052
Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn	
105 110 115	
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc	1100
Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr	
120 125 130	
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg	1148
Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met	
135 140 145	
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc	1196
Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val	
150 155 160 165	
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat	1244
Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp	
170 175 180	
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt	1292
Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg	
185 190 195	
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt	1340
Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val	
200 205 210	
cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct	1388
Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala	
215 220 225	

ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa	1436
Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu	
230 235 240 245	
atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag	1484
Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu	
250 255 260	
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc	1532
Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr	
265 270 275	
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag	1580
Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys	
280 285 290	
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc	1628
Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu	
295 300 305	
ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac	1676
Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp	
310 315 320 325	
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc	1724
Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg	
330 335 340	
atc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac	1772
Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp	
345 350 355	
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc	1820
Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile	
360 365 370	
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt	1868
Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg	
375 380 385	
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg	1916
Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu	
390 395 400 405	
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act	1964
Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr	
410 415 420	
tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg	2012
Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu	
425 430 435	
act tac aag cgt cgt ctg tcg gct ctg ggc ccg ggt ggt ctg tcc cgt	2060
Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg	
440 445 450	
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108
Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly	
455 460 465	
cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156
Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile	



470		475		480		485	
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag							2204
Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu							
		490		495		500	
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac							2252
Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp							
		505		510		515	
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac							2300
Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn							
		520		525		530	
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt							2348
Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val							
		535		540		545	
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat							2396
Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp							
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tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg							2444
Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met							
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att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg							2492
Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala							
		585		590		595	
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc							2540
Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe							
		600		605		610	
gag ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg							2588
Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu							
		615		620		625	
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc							2636
Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe							
		630		635		640	645
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt							2684
Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg							
		650		655		660	
aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg							2732
Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu							
		665		670		675	
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt							2780
Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly							
		680		685		690	
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt							2828
Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val							
		695		700		705	
gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc							2876
Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu							
		710		715		720	725

aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu 730 735 740	2924
gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile 745 750 755	2972
acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp 760 765 770	3020
gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile 775 780 785	3068
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu 790 795 800 805	3116
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg 810 815 820	3164
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly 825 830 835	3212
gag cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc Val Arg His Phe Ser Arg Glu Asp Asp Asp Leu Ala Pro Gly Val 840 845 850	3260
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp 855 860 865	3308
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys 870 875 880 885	3356
att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val 890 895 900	3404
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly 905 910 915	3452
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gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro 935 940 945	3548
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ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr 1060 1065 1070			3917
cca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly 1075 1080 1085			3962
cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro 1090 1095 1100			4007
gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu 1105 1110 1115			4052
cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr 1120 1125 1130			4097
cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly 1135 1140 1145			4142
gcc tca ctt ggc atc aac ctg tcc cgt gac gag cgt tcc gac gcc Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu Arg Ser Asp Ala 1150 1155 1160			4187
gac acc gca tagcagatca gaaaacaacc gctagaaatc aagccataca Asp Thr Ala 1165			4236
tcccccgac attgaagaga tggtctgggg ggaaaggag ttttacgtgc tcgacgtaaa			4296
cgtcttcgat gagctccgca tcggcctggc caccgccgac gacatccgcc gttggtccaa			4356
gggtgaggtc aagaagccgg agaccatcaa ctaccgaacc ctcaagcctg agaaggacgg			4416
tctgttctgc gagcgtatct tcggtccaac tcgcgactgg gagtgcgcct gcggtaaagta			4476

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cgaccgctac gaggattact tcaccggtgg tatgggtgca gagtccattg aggctttgat 5076
ccagaacttc gaccttgatg ctg 5099

210> 6

211> 1165

212> PRT

213> Corynebacterium glutamicum

400> 6

Val Leu Glu Gly Pro Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val
5 10 15

Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser
20 25 30

Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr
35 40 45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu
50 55 60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu
65 70 75 80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu
85 90 95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe
115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly
130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr
145 150 155 160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe
165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys
180 185 190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg
195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr
210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg
225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val
245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro
260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser
275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys
290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu
325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro
340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr
355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile
385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn
420 425 430

Ser Leu Ser Gly Leu Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro
435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp
530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr

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Asp 625	Ala 630	Gly 635
Val 645	Leu 650	Val 655
Thr 660	Arg 665	Gly 670
Asn 675	Gln 680	Val 685
Val 690	Ile 695	Glu 700
Arg 705	Asn 710	Gly 715
Asp 725	Ala 730	Gln 735
Ser 740	Ile 745	Arg 750
Gly 755	Ala 760	Ser 765
Leu 770	Lys 775	Val 780
Arg 785	Asp 790	Thr 795
Glu 805	Leu 810	Gly 815
Ala 820	Arg 825	Gly 830
Gly 835	Val 840	Asp 845
Leu 850	Glu 855	Tyr 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr
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Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly
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Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu
1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser
 1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe
 1130 1135 1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu
 1145 1150 1155

Arg Ser Asp Ala Asp Thr Ala
 1160 1165

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Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly
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cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc 580

Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
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cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct aag 628

Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys

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ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag			724
Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln			
60	65	70	75
gag cac tcc atg gtg ctc gtt cgc ggt ggt cgt gtt aag gac ctc cca			772
Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro			
80	85		90
ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt			820
Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val			
95	100		105
aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata			868
Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile			
110	115		120
att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct			920
ile Lys Asn Ala			
125			
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		35				40						45			

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
50 55 60

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
65 70 75 80

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
85 90 95

Le Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
100 105 110

Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala
115 120 125